

Mark D Carr

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4281720/publications.pdf>

Version: 2024-02-01

57
papers

2,695
citations

201674

27
h-index

189892

50
g-index

59
all docs

59
docs citations

59
times ranked

3491
citing authors

#	ARTICLE	IF	CITATIONS
1	Cross-Reactive SARS-CoV-2 Neutralizing Antibodies From Deep Mining of Early Patient Responses. <i>Frontiers in Immunology</i> , 2021, 12, 678570.	4.8	16
2	Conformational dynamics in interleukin 17A and 17F functional complexes is a key determinant of receptor A affinity and specificity. <i>Cytokine</i> , 2021, 142, 155476.	3.2	4
3	Discovery of a novel pseudo β^2 -hairpin structure of N-truncated amyloid- β^2 for use as a vaccine against Alzheimer's disease. <i>Molecular Psychiatry</i> , 2021, , .	7.9	11
4	Structural and functional characterization of C0021158, a high-affinity monoclonal antibody that inhibits Arginase 2 function via a novel non-competitive mechanism of action. <i>MAbs</i> , 2020, 12, 1801230.	5.2	2
5	Extensive sequence and structural evolution of Arginase 2 inhibitory antibodies enabled by an unbiased approach to affinity maturation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16949-16960.	7.1	10
6	Allosteric activation of MALT1 by its ubiquitin-binding Ig3 domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3093-3102.	7.1	14
7	<i>In Vitro</i> Assessment of Putative PD-1/PD-L1 Inhibitors: Suggestions of an Alternative Mode of Action. <i>ACS Medicinal Chemistry Letters</i> , 2019, 10, 1187-1192.	2.8	22
8	Insight into small molecule binding to the neonatal Fc receptor by X-ray crystallography and 100 kHz magic-angle-spinning NMR. <i>PLoS Biology</i> , 2018, 16, e2006192.	5.6	31
9	Structural and functional analysis of Dickkopf 4 (Dkk4): New insights into Dkk evolution and regulation of Wnt signaling by Dkk and Kremen proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 12149-12166.	3.4	26
10	Structure of a Potential Therapeutic Antibody Bound to Interleukin-16 (IL-16). <i>Journal of Biological Chemistry</i> , 2016, 291, 16840-16848.	3.4	11
11	Resonance assignment and secondary structure determination of full length human Dickkopf 4 (hDkk4), a secreted, disulphide-rich Wnt inhibitor protein. <i>Biomolecular NMR Assignments</i> , 2015, 9, 147-151.	0.8	2
12	Conformational Heterogeneity in Antibody-Protein Antigen Recognition. <i>Journal of Biological Chemistry</i> , 2014, 289, 7200-7210.	3.4	13
13	^{15}N , ^{13}C and ^1H resonance assignments and secondary structure determination of a variable heavy domain of a heavy chain antibody. <i>Biomolecular NMR Assignments</i> , 2014, 8, 113-116.	0.8	2
14	The Discovery, Engineering and Characterisation of a Highly Potent Anti-Human IL-13 Fab Fragment Designed for Administration by Inhalation. <i>Journal of Molecular Biology</i> , 2013, 425, 577-593.	4.2	33
15	<i>Mycobacterium tuberculosis</i> RNA Polymerase-binding Protein A (RbpA) and Its Interactions with Sigma Factors. <i>Journal of Biological Chemistry</i> , 2013, 288, 14438-14450.	3.4	44
16	Structure and Interactions of the Human Programmed Cell Death 1 Receptor. <i>Journal of Biological Chemistry</i> , 2013, 288, 11771-11785.	3.4	256
17	Characterization of the Interaction of Sclerostin with the Low Density Lipoprotein Receptor-related Protein (LRP) Family of Wnt Co-receptors. <i>Journal of Biological Chemistry</i> , 2012, 287, 26464-26477.	3.4	77
18	Conservation of Functional Sites on Interleukin-6 and Implications for Evolution of Signaling Complex Assembly and Therapeutic Intervention. <i>Journal of Biological Chemistry</i> , 2012, 287, 40043-40050.	3.4	20

#	ARTICLE	IF	CITATIONS
19	The statistical significance of selected sense-antisense peptide interactions. <i>Journal of Computational Chemistry</i> , 2012, 33, 1440-1447.	3.3	5
20	Interaction of the Transactivation Domain of B-Myb with the TAZ2 Domain of the Coactivator p300: Molecular Features and Properties of the Complex. <i>PLoS ONE</i> , 2012, 7, e52906.	2.5	7
21	Structure of the Tandem MA-3 Region of Pcd4 Protein and Characterization of Its Interactions with eIF4A and eIF4G. <i>Journal of Biological Chemistry</i> , 2011, 286, 17270-17280.	3.4	29
22	Solution Structure of the Mycobacterium tuberculosis EsxG-EsxH Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 29993-30002.	3.4	77
23	Resonance assignment and secondary structure of the middle MA-3 domain and complete tandem MA-3 region of the tumour suppressor protein Pcd4. <i>Biomolecular NMR Assignments</i> , 2010, 4, 49-53.	0.8	2
24	Characterization of the Structural Features and Interactions of Sclerostin. <i>Journal of Biological Chemistry</i> , 2009, 284, 10890-10900.	3.4	206
25	High Resolution NMR-based Model for the Structure of a scFv-IL-1 β Complex. <i>Journal of Biological Chemistry</i> , 2009, 284, 31928-31935.	3.4	40
26	¹⁵ N, ¹³ C and ¹ H resonance assignments and secondary structure determination of the Mycobacterium tuberculosis Rv0287-Rv0288 protein complex. <i>Biomolecular NMR Assignments</i> , 2009, 3, 171-174.	0.8	6
27	Structural characterization of the interaction of mTOR with phosphatidic acid and a novel class of inhibitor: compelling evidence for a central role of the FRB domain in small molecule-mediated regulation of mTOR. <i>Oncogene</i> , 2008, 27, 585-595.	5.9	138
28	Molecular Features Governing the Stability and Specificity of Functional Complex Formation by Mycobacterium tuberculosis CFP-10/ESAT-6 Family Proteins. <i>Journal of Biological Chemistry</i> , 2008, 283, 17681-17690.	3.4	48
29	Structure of the C-terminal MA-3 domain of the tumour suppressor protein Pcd4 and characterization of its interaction with eIF4A. <i>Oncogene</i> , 2007, 26, 4941-4950.	5.9	45
30	NMR Assignment of the mTOR Domain Responsible for Rapamycin Binding. <i>Journal of Biomolecular NMR</i> , 2006, 36, 3-3.	2.8	31
31	NMR Assignment and Secondary Structure Determination of the C-terminal MA-3 Domain of the Tumour Suppressor Protein Pcd4. <i>Journal of Biomolecular NMR</i> , 2006, 36, 18-18.	2.8	8
32	Structural Diversity in p160/CREB-binding Protein Coactivator Complexes. <i>Journal of Biological Chemistry</i> , 2006, 281, 14787-14795.	3.4	67
33	Structure and function of the complex formed by the tuberculosis virulence factors CFP-10 and ESAT-6. <i>EMBO Journal</i> , 2005, 24, 2491-2498.	7.8	282
34	Superior T cell activation by ESAT-6 as compared with the ESAT-6-CFP-10 complex. <i>International Immunology</i> , 2005, 17, 1439-1446.	4.0	26
35	Characterisation of complex formation between members of the Mycobacterium tuberculosis complex CFP-10/ESAT-6 protein family: towards an understanding of the rules governing complex formation and thereby functional flexibility. <i>FEMS Microbiology Letters</i> , 2004, 238, 255-262.	1.8	42
36	Letter to the Editor: Sequence-specific assignment and secondary structure determination of the 195-residue complex formed by the Mycobacterium tuberculosis proteins CFP-10 and ESAT-6. <i>Journal of Biomolecular NMR</i> , 2004, 30, 225-226.	2.8	33

#	ARTICLE	IF	CITATIONS
37	Characterisation of complex formation between members of the complex CFP-10/ESAT-6 protein family: towards an understanding of the rules governing complex formation and thereby functional flexibility. <i>FEMS Microbiology Letters</i> , 2004, 238, 255-262.	1.8	39
38	Sequence-specific assignment of the B-Myb DNA-binding domain (B-MybR2R3) bound to a 16 base-pair DNA target site corresponding to a regulatory site from the tom-1 gene. <i>Journal of Biomolecular NMR</i> , 2003, 26, 375-376.	2.8	0
39	Solution Structure of the Mycobacterium tuberculosis Complex Protein MPB70. <i>Journal of Biological Chemistry</i> , 2003, 278, 43736-43743.	3.4	48
40	Conclusive Evidence That the Major T-cell Antigens of the Mycobacterium tuberculosis Complex ESAT-6 and CFP-10 Form a Tight, 1:1 Complex and Characterization of the Structural Properties of ESAT-6, CFP-10, and the ESAT-6- Δ -CFP-10 Complex. <i>Journal of Biological Chemistry</i> , 2002, 277, 21598-21603.	3.4	288
41	High-Resolution Solution Structure of Human Intestinal Trefoil Factor and Functional Insights from Detailed Structural Comparisons with the Other Members of the Trefoil Family of Mammalian Cell Motility Factors. <i>Biochemistry</i> , 2001, 40, 9552-9559.	2.5	23
42	Sequence-specific assignment and determination of the secondary structure of the 163-residue M. tuberculosis and M. bovis antigenic protein mpb70. <i>Journal of Biomolecular NMR</i> , 2001, 20, 185-186.	2.8	2
43	Tyrosine 36 Plays a Critical Role in the Interaction of the AB Loop of Tissue Inhibitor of Metalloproteinases-2 with Matrix Metalloproteinase-14. <i>Journal of Biological Chemistry</i> , 2001, 276, 32966-32970.	3.4	39
44	The Effect of Matrix Metalloproteinase Complex Formation on the Conformational Mobility of Tissue Inhibitor of Metalloproteinases-2 (TIMP-2). <i>Journal of Biological Chemistry</i> , 1999, 274, 37226-37232.	3.4	21
45	¹ H NMR structure of an antifungal β -thionin protein SÎ±1: Similarity to scorpion toxins. , 1998, 32, 334-349.		36
46	Solution Structure of the B-Myb DNA-Binding Domain: A Possible Role for Conformational Instability of the Protein in DNA Binding and Control of Gene Expression. <i>Biochemistry</i> , 1998, 37, 9619-9629.	2.5	24
47	High Resolution Structure of the N-terminal Domain of Tissue Inhibitor of Metalloproteinases-2 and Characterization of Its Interaction Site with Matrix Metalloproteinase-3. <i>Journal of Biological Chemistry</i> , 1998, 273, 21736-21743.	3.4	80
48	Mapping the Binding Site for Matrix Metalloproteinase on the N-Terminal Domain of the Tissue Inhibitor of Metalloproteinases-2 by NMR Chemical Shift Perturbation. <i>Biochemistry</i> , 1997, 36, 13882-13889.	2.5	119
49	Chemically and Conformationally Authentic Active Domain of Human Tissue Inhibitor of Metalloproteinases-2 Refolded from Bacterial Inclusion Bodies. <i>FEBS Journal</i> , 1996, 241, 476-483.	0.2	39
50	Structure of the B-Myb DNA-binding Domain in Solution and Evidence for Multiple Conformations in the Region of Repeat-2 Involved in DNA Binding. Implications for Sequence-Specific DNA Binding by Myb Proteins. <i>FEBS Journal</i> , 1996, 235, 721-735.	0.2	28
51	NMR-Based Structural Studies of the pNR-2/pS2 Single Domain Trefoil Peptide. Similarities to Porcine Spasmolytic Peptide and Evidence for a Monomeric Structure. <i>FEBS Journal</i> , 1995, 233, 847-855.	0.2	18
52	Solution structure of the active domain of tissue inhibitor of metalloproteinases-2. A new member of the OB fold protein family. <i>Biochemistry</i> , 1994, 33, 11745-11759.	2.5	106
53	Proton NMR-based determination of the secondary structure of porcine pancreatic spasmolytic polypeptide: one of a new family of "trefoil" motif containing cell growth factors. <i>Biochemistry</i> , 1992, 31, 1998-2004.	2.5	49
54	The transcriptional control proteins c-Myb and v-Myb contain a basic region DNA binding motif. <i>FEBS Letters</i> , 1991, 282, 293-294.	2.8	14

#	ARTICLE	IF	CITATIONS
55	NMR and molecular dynamics studies of the mKr2 'zinc finger'. FEBS Journal, 1990, 188, 455-461.	0.2	19
56	The ¹ H-NMR assignments of the aromatic resonances in complexes of Lactobacillus casei dihydrofolate reductase and the origins of their chemical shifts. FEBS Journal, 1990, 191, 659-668.	0.2	10
57	Nucleotide binding to active and 4-chloro-7-nitrobenzofurazan-inhibited forms of chloroplast F1-ATPase – an NMR study. Biochimica Et Biophysica Acta - Bioenergetics, 1990, 1015, 79-86.	1.0	5